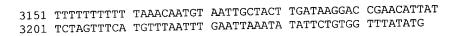




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51	TCARCARCA	CTTCAACCCC	ATGAAGCAGC	TGGCTAACCA	GACCGTGGGC
101	AGAGCTGAGA		CCTTACTCAA	GATCTATTAC	AGATTGAGAG
				CCATTCCCAT	
201				ATGCCGAGAG	
251	TGGCATGTTT		TO CTO A A A A T	ATGCAAGAAG	CATCGACTCA
301	AAACTGCCTC			GGAGACGTGT	
351	GCTGGAAGAC	TCTCTCCTGG			
401	AGAATCAGCT	GGCTCTCGAG	CTCTCCCAGC		TGTTGAGAAG
451			CGGCATAGCT	GAGGTGGAGA	TTCCCAACAT
501			TTGCAAGATT		TGGGATTCAG
551	TCAGAGCCAG	GTGGAACCAA	GCTCACAAAT	CCTCAGGAAC	CAACTTTCAG
601	GGGCTTCCAT	CAAAAATAGA	TACTCTAAAG	GAAGAGATGG	ATGAAGCTGG
651				TGCAGCAGAC	ATGTACAACT
701	TTATGGCCAA	AGAAGGGGAG		TCTTTGTTAC	
751	GCCCAAGCAG	ATTACCATAG	AAAAGCATTA	GCAGTCTTAG	AAAAGACCCT
801		CGAGCCCATC		GGCGGAAAAA	
851	GGACTCCCCT	AGCAGAACAC	CTGAAGAGGA	GCGGGCGCGA	
901		CCTGTGTCAT		GAGACAGGCA	TGAAGGAGGA
951	GGGCCTTTTC		CTGGGGCCTC	CAAGTTAAAG	AAGCTGAAAG
1001	CTGCTTTGGA		TCTCACCTGG	ATGAGTTCTA	TTCAGACCCC
1051	CATGCTGTAG			TTACGGGAAT	
1101	TTTGATGACT	TTTAATCTGT	ATGAAGAATG	GACACAAGTT	GCAAGTGTGC
	AGGATCAAGA		CAAGACTTGT	GGAGAACATG	
1101	CCACCACAAA	λ π π π π α π α τ α Δ Δ			
	GCTTGCTCAG	ACCAGCGATG	TGAATAAAAT		AACATTGCGA
1251		CCCTAACTTG		GAAATGAAGG	
	TTGTGTTAGG		CGTCCATGTG		TTGAACCCAT
	GAAATGGCAG			AGAGGTGGAA	TTTAATGTAT
	CATTCAGCAT			GTTCTAATCA	
1451	CAGAAGCATT	TGTACCTCTC	ACCACCCGA	GAGAGGAAGC	CCCCTCCTAG
1501	ACTGGAAACG	ACTCTGACTC	CGGGACCCTG	CARCCAAACC	CCTCCCAAAC
1551	CATGGCGGTG	ATGGAAGGAG	ACTIGGIGAA	GAAGGAAAGT	AAACAACACT
1601		TGTATCTGCA	GCTGTGCCAG	CACCAGGGAG	CCTCCCACCA
1651	CAGATAGCAT	CTGGCCAAAA	TCAGCCCCAG	GCAGCTGCTG	GCTCCCACCA
1701		GGCCAACCTC	ACAATGCTGC	AGGGCCCAGC	TOGGGGGGAACAC
1751				CACCCCGAA	ACCGGGCAAC
1801	CCACCTCCTG	GCCACCCCGG	GGGCCAGAGT		CATCTCAGCA
1851	TCCACCCAGT	CTGTCACCAA	AGCCACCCAC		TCTCCTCCCA
1901	CCCAGCACAC	GGGCCAGCCT	CCAGGCCAGC		CTCCCAGCTC
1951	TCAGCACCCC				AAGCTCCCAA
2001			CTACGCAGGC		ATGCACACCA
2051	AACCCAATAG	CCAGGGCCCT	CCCAACCCCA		CAGTGAGCAT
2101	GGACTTGAGC	AGCCATCTCA	CACCCCTCCC	CAGACTCCAA	CGCCCCCAG
2151	TACTCCGCCC	CTAGGAAAAC	AGAACCCCAG	TCTGCCAGCT	CCTCAGACCC
2201	TGGCAGGGGG	TAACCCTGAA	ACTGCACAGC	: CACATGCTGG	AACCTTACCG
2251	AGACCGAGAC	CAGTACCAAA	GCCAAGGAAC	CGGCCCAGCG	TGCCCCCACC
2301	CCCCCAACCT	CCTGGTGTCC	ACTCAGCTGG	GGACAGCAGC	CTCACCAACA
2351	CAGCACCAAC	: AGCTTCCAAG	ATAGTAACAG	ACTCCAATTC	CAGGGTTTCA
2401	GAACCGCATC	GCAGCATCTT	TCCTGAAATG	CACTCAGACT	CAGCCAGCAA
2451	AGACGTGCCT	GGCCGCATCC	TGCTGGATAT	' AGACAATGAT	ACCGAGAGCA
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2551	CGAGTGGAGC	AGGGGCAGGC	GAACCTCTT	CTTTGCAGAC	CGAACAGTGA
2601	AAAGCTTTCA	GTGGAGGACA	AAGGAGGCC	CTCACTGTGCG	GGACCTGGCC
2651	TTCTGCACGG	CCCAAGGAGA	ACCTGGAGGC	CACCACTAAA	GCTGAATGAC
2701	. 110100/1000 	AAGAAGTTGG	CTTTCTTTAC	ATGGGAAGGA	AATCATGCCA
2751	στοισισίτος	AAACAAAGAA	GTACCTGGAG	TGGAGAGAGT	ATTCCTGCTG
2/31	AAAAAAAICCE	· ACCAACCTT	TGTCCCTGCT	GTTAATGCGG	GCAGCACCTA
2001	CACCAACTT	. AUUAAUUIII 2 CAATCACTA	GAAGCAGTGO	GTTAACTATO	TATTTAATAA
2001	L CAGCAACTTC	, AUVIGURIE 2 GUVIGURE	, CCCCTACTG	CTGCTACCTC	GACGTTCATT
2901	L AAIGUGUTUA	A TIMIGUMAGI	CTCCCCCCCC	T TCAGACTTGC	TGCAGAATCA
295	L CTTATGTATT	AGGAGGGAGG	3 CIGCGCICCI	Z AGTOCOCOTO	GAACCATGCC
3001	L TTTTGTATCA	A TGTATGGTCT	. GIGICICCC . TCTCTCTCTCTCT	P CATCANACTO	GATGTGACCC
3051	L CATGGATGGT	GACTGCTGGC	COCARRORA	L CHICHMACIC	GATGTGACCC
3101	L ATGCCGCCTC	J GTTGGATTGT	CGGAATGTAC	ACHGAAATG1	ACTGTTCTTT



#### FEATURES:

5'UTR: 1-99 Start Codon: 100 Stop Codon: 2509 3'UTR: 2512

### Homologous proteins:

Homologods processo.		
Top 10 BLAST Hits	Score	E
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CRA 147000022595308 /altid=gi 10435148 /def=dbj DDF1700011 na CRA 335001098671246 /altid=gi 11560044 /def=ref NP_071580.1  na	1331	0.0
CRA 335001098671246 /altid=gi 71500044 /def=fef NP_055674.1  KIAA CRA 18000005158484 /altid=gi 7662242 /def=ref NP_055674.1  KIAA	645	0.0
CRA 18000005158484 /aitid=gi /1602242 /def=fef KF_008288.1  KI CRA 335001098684832 /altid=gi 11425473 /def=ref XF_008288.1  KI	645	0.0
CRA 335001098684832 /altid=gi 11425475 /def=ref RP_007992.1  hy CRA 335001098688185 /altid=gi 11431577 /def=ref RP_007992.1  hy	452	e-126
CRA 335001098688185 /altid=gi 1151577 /def ref NP_061830.1  SH CRA 335001098646266 /altid=gi 11545733 /def=ref NP_061830.1  SH	421	e-116
CRA 335001098646266 /altid=gi 11343/3 /def left NP_033190.1  SH3 CRA 18000004990129 /altid=gi 6677931 /def=ref NP_033190.1  SH3	390	e-107
CRA 18000004990129 /altid=g1 007/351 /def left 12   CRA 89000000202138 /altid=g1 7300563 /def=gb AAF55715.1  (AE003	264	3e-69
CRA 66000019404309 /altid=gi 8922344 /def=ref NP_060524.1  homo	251	2e-65
CRA 1800000194043039 /altid=gi 7512523 /def=pir  T12533 hypotheti	190	4e-47
EST: qi 10993873 /dataset=dbest /taxon=96	1524	0.0
qi 11003732 /dataset=dbest /taxon=96	1495	0.0
gi 12040806 /dataset=dbest /taxon=96	1170	0.0
gi 10948137 /dataset=dbest /taxon=96	1049	0.0
qi 11303345 /dataset=dbest /taxon=96	1043	0.0
gi 7933255 /dataset=dbest /taxon=960	918	0.0
gi 10332226 /dataset=dbest /taxon=96	912	0.0
gi 11643637 /dataset=dbest /taxon=96	906	0.0
qi 10348166 /dataset=dbest /taxon=960	664	0.0
gi 4753575 /dataset=dbest /taxon=9606	609	e-171

# EXPRESSION INFORMATION FOR MODULATORY USE:

## library source:

```
Expression information from BLAST dbEST hits:

gi|10993873 Neuronal teratocarcinoma
gi|11003732 Umbilical vein endothelial cell
gi|12040806 Iris
gi|10948137 Teratocarcinoma
gi|11303345 Breast
gi|7933255 Leiomios
gi|10332226 Uterus
gi|11643637 Kidney renal carcinoma (ascites)
gi|10348166 Uterus leiomyosarcoma
gi|4753575 Human fetal heart
```

Expression information from PCR-based tissue screening panels: Human leukocytes

```
1 MKKQFNRMKQ LANQTVGRAE KTEVLSEDLL QIERRLDTVR SICHHSHKRL
51 VACFQGQHGT DAERRHKKLP LTALAQNMQE ASTQLEDSLL GKMLETCGDA
101 ENQLALELSQ HEVFVEKEIV DPLYGIAEVE IPNIQKQRKQ LARLVLDWDS
151 VRARWNQAHK SSGTNFQGLP SKIDTLKEEM DEAGNKVEQC KDQLAADMYN
201 FMAKEGEYGK FFVTLLEAQA DYHRKALAVL EKTLPEMRAH QDKWAEKPAF
251 GTPLAEHLKR SGREIALPIE ACVMLLLETG MKEEGLFRIG AGASKLKKLK
301 AALDCSTSHL DEFYSDPHAV AGALKSYLRE LPEPLMTFNL YEEWTQVASV
351 QDQDKKLQDL WRTCQKLPPQ NFVNFRYLIK FLAKLAQTSD VNKMTPSNIA
401 IVLGPNLLWA RNEGTLAEMA AATSVHVVAV IEPIIQHADW FFPEEVEFNV
451 SEAFVPLTTP SSNHSFHTGN DSDSGTLERK RPASMAVMEG DLVKKESPPK
501 PKDPVSAAVP APGRNNSQIA SGQNQPQAAA GSHQLSMGQP HNAAGPSPHT
551 LRRAVKKPAP APPKPGNPPP GHPGGQSSSG TSQHPPSLSP KPPTRSPSPP
601 TQHTGQPPGQ PSAPSQLSAP RRYSSSLSPI QAPNHPPPQP PTQATPLMHT
651 KPNSQGPPNP MALPSEHGLE QPSHTPPQTP TPPSTPPLGK QNPSLPAPQT
701 LAGGNPETAQ PHAGTLPRPR PVPKPRNRPS VPPPPQPPGV HSAGDSSLTN
751 TAPTASKIVT DSNSRVSEPH RSIFPEMHSD SASKDVPGRI LLDIDNDTES
801 TAL
```

#### FEATURES:

# Functional domains and key regions:

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION N-glycosylation site

```
Number of matches: 6

1 13-16 NQTV
2 449-452 NVSE
3 463-466 NHSF
4 470-473 NDSD
5 515-518 NNSQ
6 796-799 NDTE
```

[2] PDOC00004 PS00004 CAMP\_PHOSPHO\_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site

```
Number of matches: 2
1 494-497 KKES
2 621-624 RRYS
```

[3] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site

```
Number of matches: 7
1 38-40 TVR
2 46-48 SHK
3 150-152 SVR
4 175-177 TLK
5 261-263 SGR
6 550-552 TLR
7 589-591 SPK
```

[4] PDOC00006 PS00006 CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site

```
Number of matches: 14
             60-63 TDAE
      1
             83-86 TQLE
            96-99 TCGD
      3
           109-112 SQHE
      4
           171-174 SKID
           175-178 TLKE
      6
           214-217 TLLE
      7
           233-236 TLPE
      8
           261-264 SGRE
           308-311 SHLD
     10
           349-352 SVQD
           415-418 TLAE
     12
           468-471 TGND
     13
           742-745 SAGD
     14
```

[5] PDOC00007 PS00007 TYR\_PHOSPHO\_SITE Tyrosine kinase phosphorylation site

## 117-124 KEIVDPLY

[6] PDOC00008 PS00008 MYRISTYL N-myristoylation site

```
Number of matches: 10
           56-61 GQHGTD
           251-256 GTPLAE
         290-295 GAGASK
          322-327 GALKSY
          538-543 GQPHNA
      5
           574-579 GGQSSS
      6
      7
           575-580 GQSSSG
           605-610 GQPPGQ
      8
           704-709 GNPETA
      9
           739-744 GVHSAG
     10
```

[7] PDOC00161 PS00178 AA\_TRNA\_LIGASE\_I Aminoacyl-transfer RNA synthetases class-I signature

## 706-716 PETAQPHAGTL

# Membrane spanning structure and domains: Helix Begin End Score Certainty 1 415 435 0.842 Putative



>CRA|147000022595308 /altid=gi|10435148 /def=dbj|BAB14506.1| (AK023281) unnamed protein product [Homo sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa /length=726 Length = 726

Score = 1500 bits (3840), Expect = 0.0Identities = 726/726 (100%), Positives = 726/726 (100%)

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>CRA|335001098671246 /altid=gi|11560044 /def=ref|NP\_071580.1|

nadrin; neuron-specific GTPase activating protein
[Rattus norvegicus] /org=Rattus norvegicus /taxon=10116
/dataset=nraa /length=780
Length = 780

Score = 1331 bits (3406), Expect = 0.0Identities = 676/816 (82%), Positives = 697/816 (84%), Gaps = 49/816 (6%) MKKQFNRMKQLANQTVGRAEKTEVLSEDLLQIERRLDTVRSICHHSHKRLVACFQGQHGT 60 Query: 1 MKKQFNRMKQLANQTVGRAEKTEVLSEDLLQIERRLDTVRS+CHHSHKRL+ACFQGQHGT MKKQFNRMKQLANQTVGRAEKTEVLSEDLLQIERRLDTVRSMCHHSHKRLIACFQGQHGT 60 Sbjct: 1 Query: 61 DAERRHKKLPLTALAQNMQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEKEIV 120 DAERRHKKLPLTALAQNMQEAS QLE+SLLGKMLETCGDAENQLA ELSQHEVFVEKEI+ Sbjct: 61 DAERRHKKLPLTALAQNMQEASAQLEESLLGKMLETCGDAENQLAFELSQHEVFVEKEIM 120 Query: 121 DPLYGIAEVEIPNIQKQRKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEM 180 DPLYGIAEVEIPNIQKQRKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEM Sbjct: 121 DPLYGIAEVEIPNIQKQRKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEM 180 Query: 181 DEAGNKVEQCKDQLAADMYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAH 240 DEAGNKVEQCKDQLAADMYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEK LPEMRAH Sbjct: 181 DEAGNKVEQCKDQLAADMYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKALPEMRAH 240 Query: 241 QDKWAEKPAFGTPLAEHLKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLK 300 QDKWAEKPAFGTPL EHLKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLK Sbjct: 241 QDKWAEKPAFGTPLEEHLKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLK 300 Query: 301 AALDCSTSHLDEFYSDPHAVAGALKSYLRELPEPLMTFNLYEEWTQVASVQDQDKKLQDL 360 AALDCSTSHLDEFYSDPHAVAGALKSYLRELPEPLMTF+LYEEWTQVASVQDQDKKLQ L Sbjct: 301 AALDCSTSHLDEFYSDPHAVAGALKSYLRELPEPLMTFSLYEEWTQVASVQDQDKKLQYL 360 Query: 361 WRTCQKLPPQNFVNFRYLIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWARNEGTLAEMA 420 W TCQKLPPQNFVNFRYLIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWA+ EGTLAE+A Sbjct: 361 WTTCQKLPPQNFVNFRYLIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWAKQEGTLAEIA 420 Query: 421 AATSVHVVAVIEPIIQHADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERK 480 AATSVHVVAVIEPIIQHADWFFP EVEFNVSEAFVPL TP+SNHS HTGNDSDSGTLERK Sbjct: 421 AATSVHVVAVIEPIIQHADWFFPGEVEFNVSEAFVPLATPNSNHSSHTGNDSDSGTLERK 480 Query: 481 RPASMAVMEGDLVKKESPPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQP 540 RPASMAVMEGDLVKKESPPKPKD VSAA P GRN++QI + NQ Q Sbjct: 481 RPASMAVMEGDLVKKESPPKPKDSVSAAAPVAGRNSNQITTVPNQAQTGGNSHQLSVGTA 540 Query: 541 HNAAGPSPHTLRRAVKKPAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPP 600 H+AAGPSPHTLRRAVKKPAPAPPKPGNPPPGHPGGQSS GT SPKP TRSPSPP Sbjct: 541 HSAAGPSPHTLRRAVKKPAPAPPKPGNPPPGHPGGQSSPGT----GTSPKPSTRSPSPP 595 Query: 601 -----TQHTGQPPGQPSAPSQLSAPRRYSSSLSPIQAPNHPPPQPPTQATPL 647 Q Q Q RR SSSL PIQAPNHPPPQPPTQ Query: 648 MHTKPNSQGPPNPMALPSEHGLEQPSHTPPQTPTPPSTPPLGKQNPSLPAPQTLAGGNPE 707 +P TPPQTPTPPSTPP KQN S + OGP Sbjct: 652 --PRLGEQGP------EPGPTPPQTPTPPSTPPPAKQNSS-----QSE 686 Query: 708 TAQPHAGTLPRPRPVPKPRNRPSVPPPPQPPGVHSAGDSSLTNTAPTASKIVTDSNSRVS 767 T Q H GTLPRPRPVPKPRNRPSVPPPP PPG H GD LT + PTAS+IVTD+NSRVS Sbjct: 687 TTQLH-GTLPRPRPVPKPRNRPSVPPPPNPPGTH-MGDGGLTPSVPTASRIVTDTNSRVS 744 Query: 768 EPHRSIFPEMHSDSASKDVPGRILLDIDNDTESTAL 803 E R+IFPE+HSD ASK+VPG ILLDIDNDTESTAL Sbjct: 745 ESLRNIFPEIHSDLASKEVPGHILLDIDNDTESTAL 780

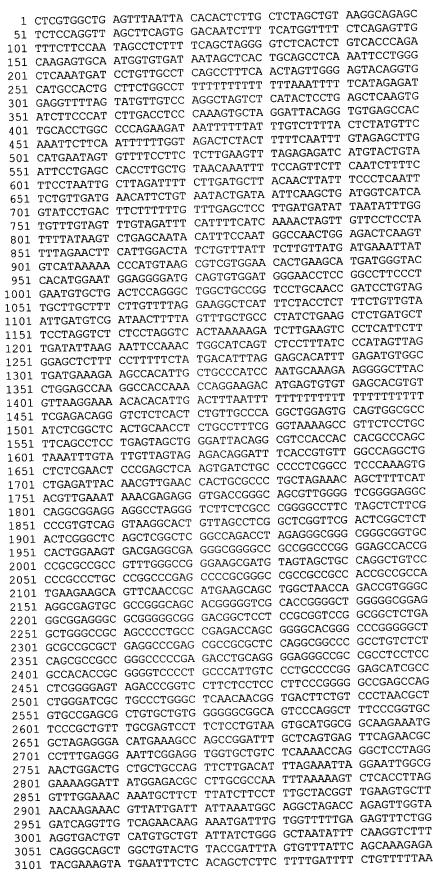
Hmmer search results (Pfam):

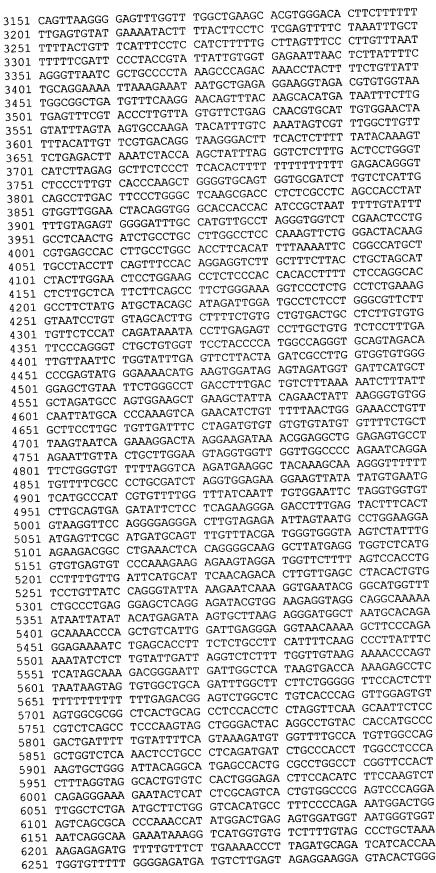
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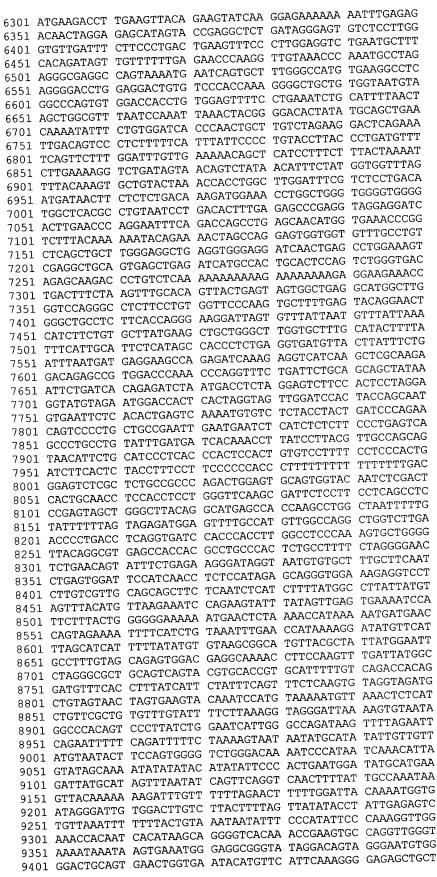
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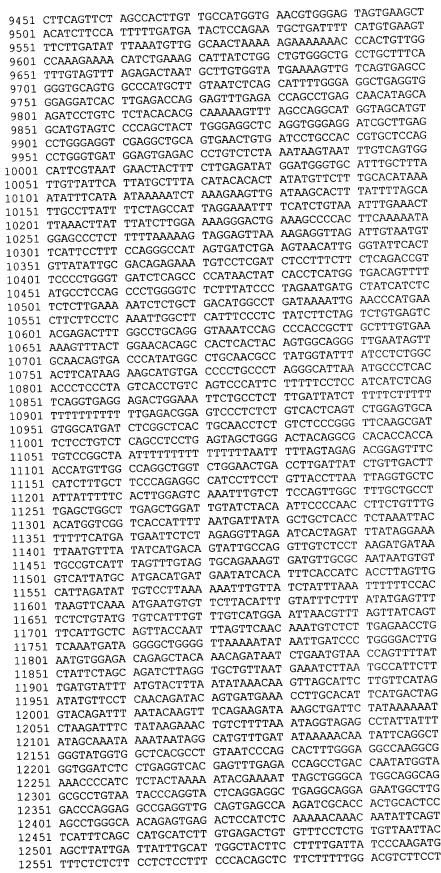
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 Domain
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 seq-t
 hmm-f
 hmm-t
 score
 E-value

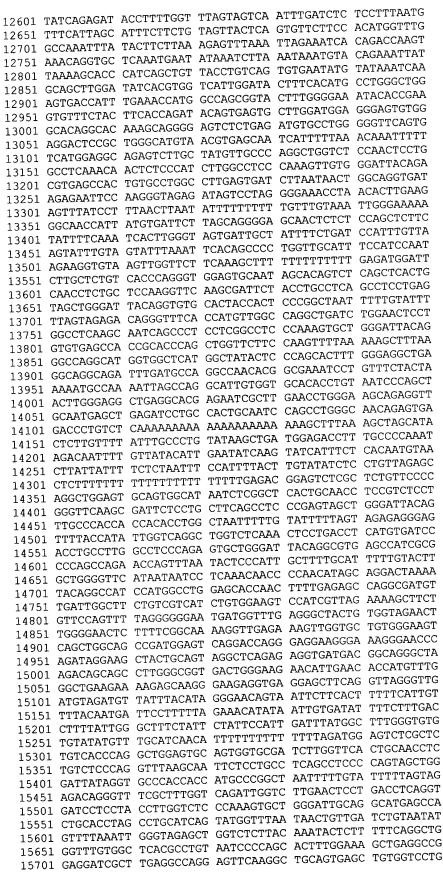
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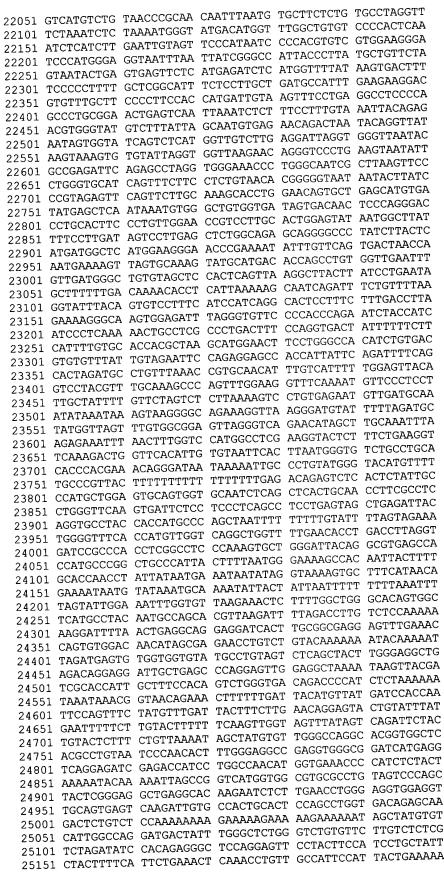


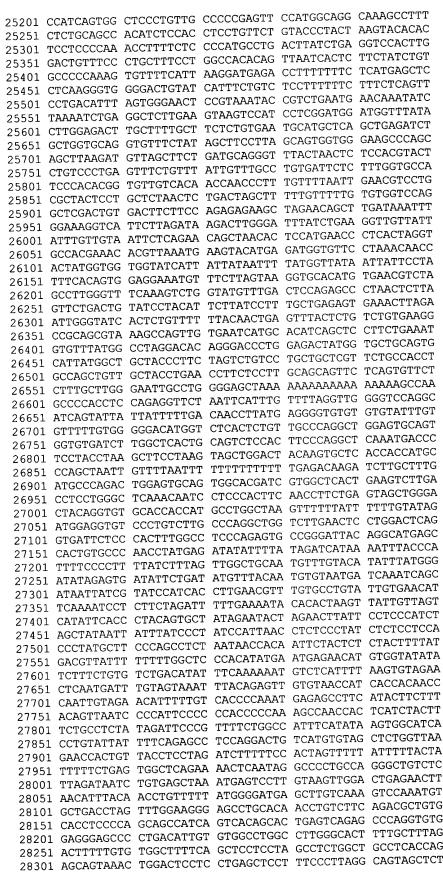




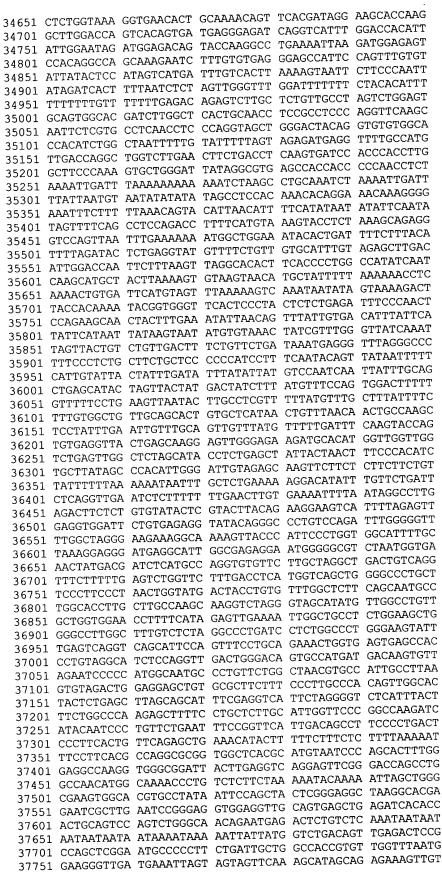
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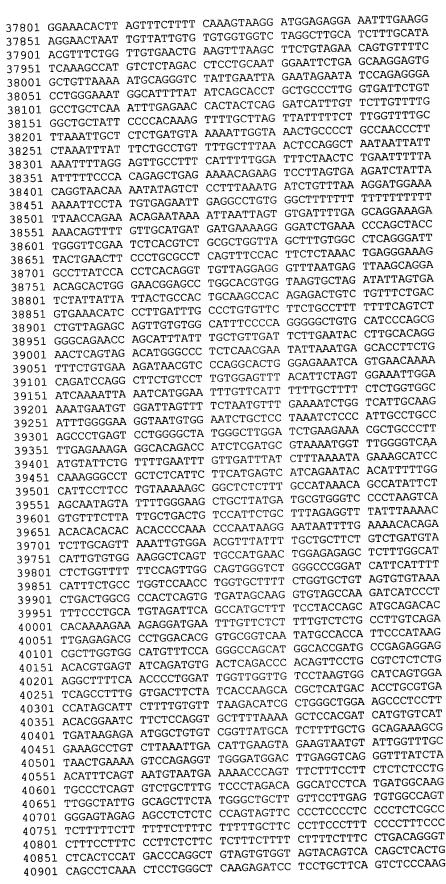


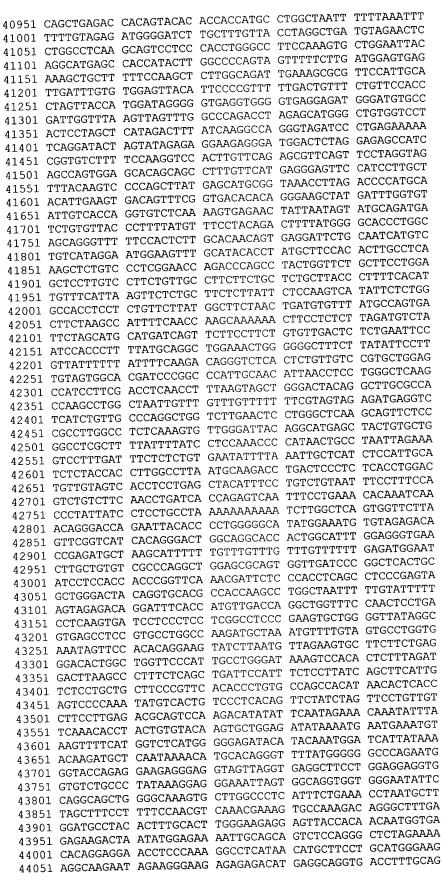


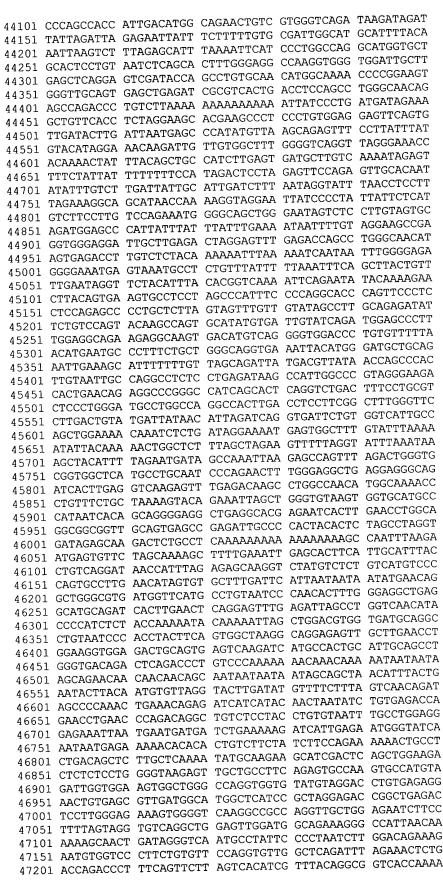


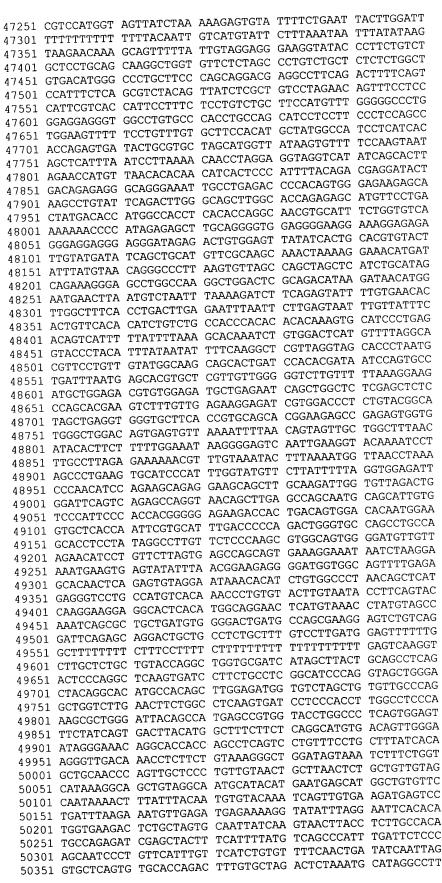
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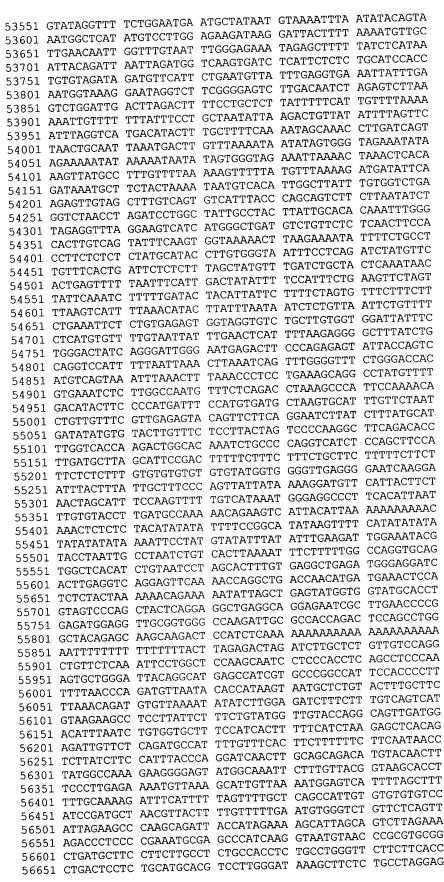


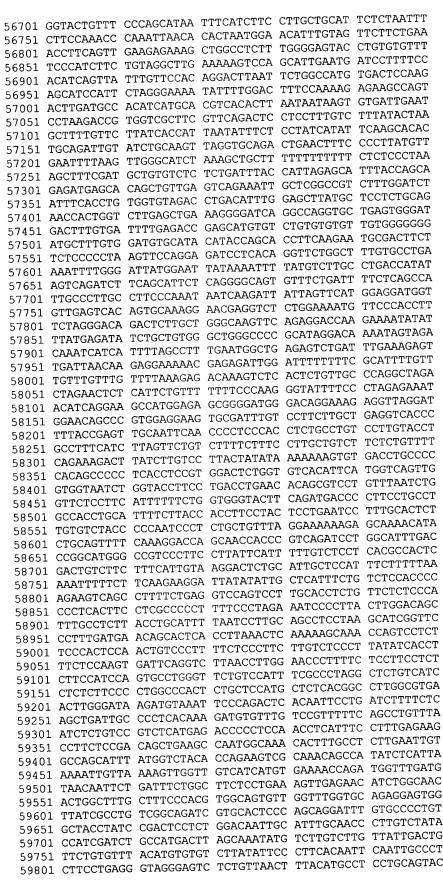


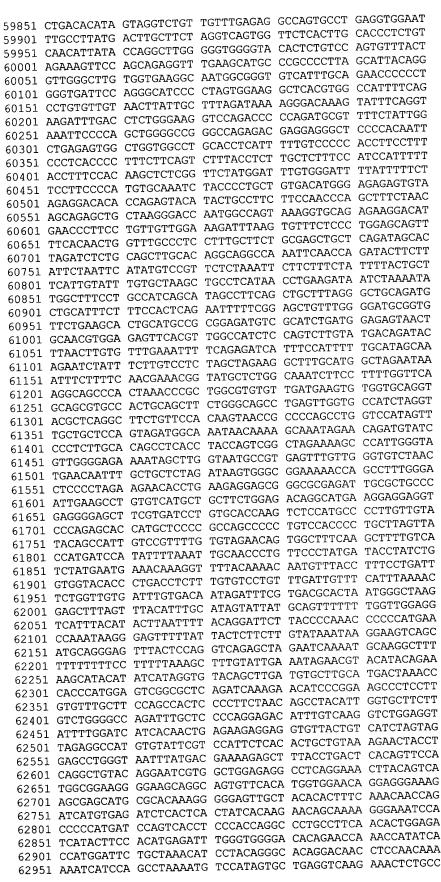


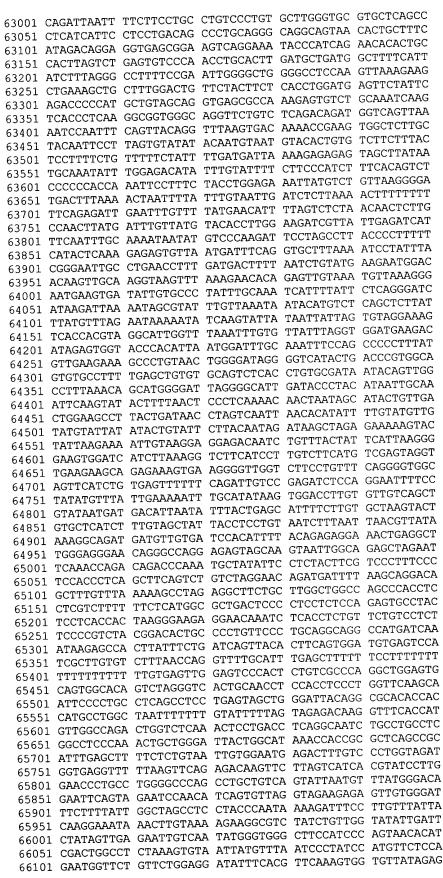


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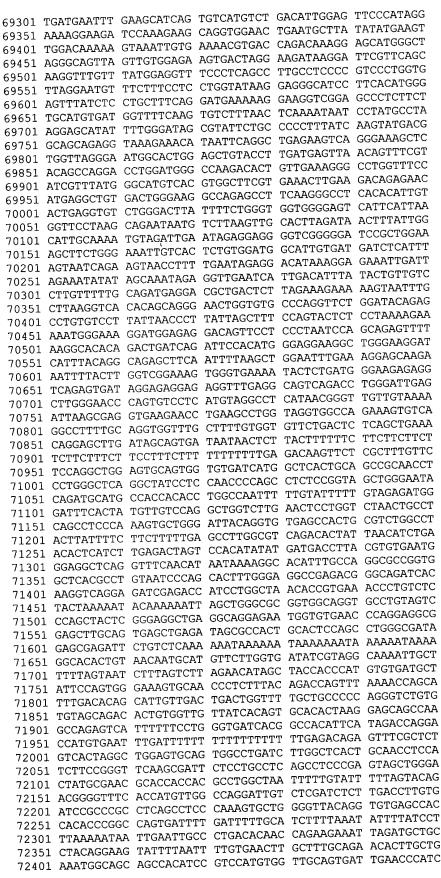


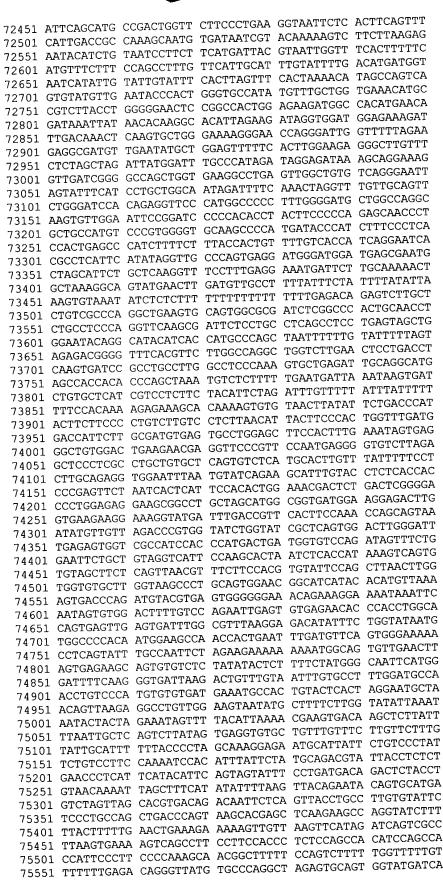


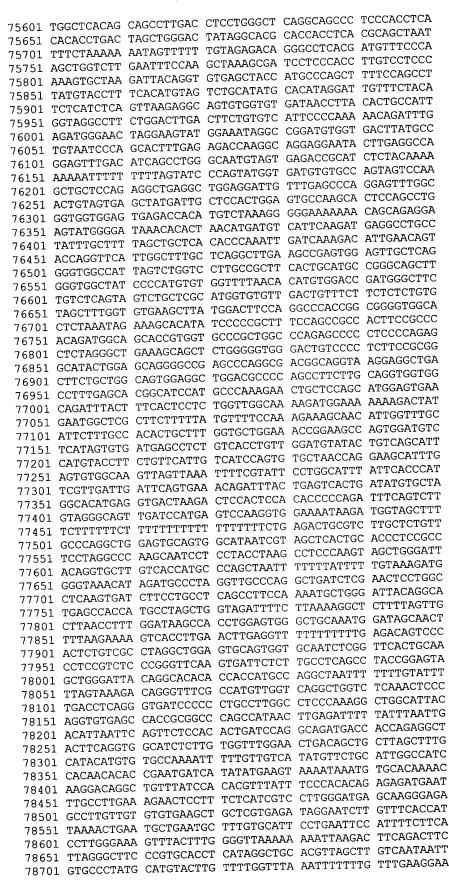


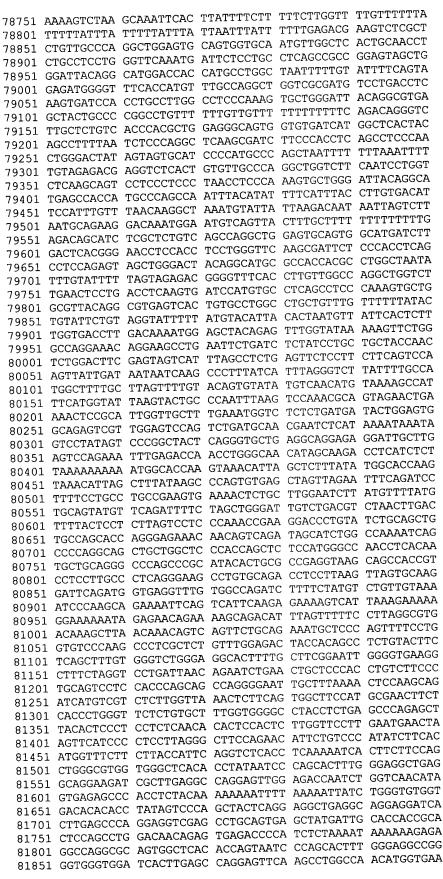


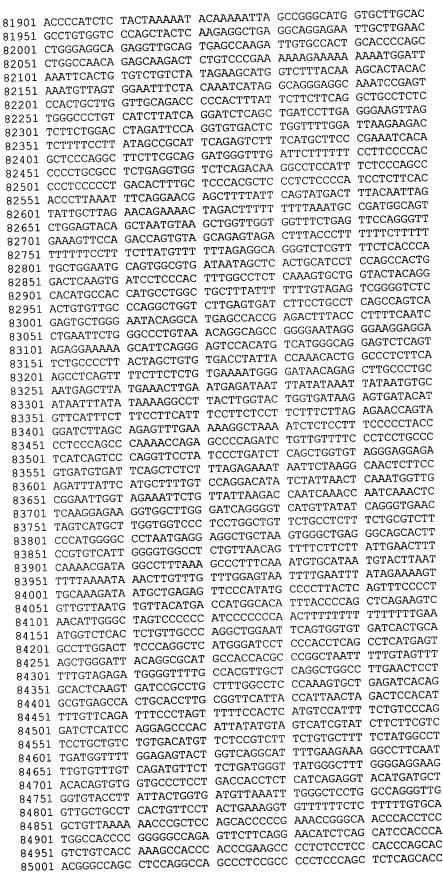
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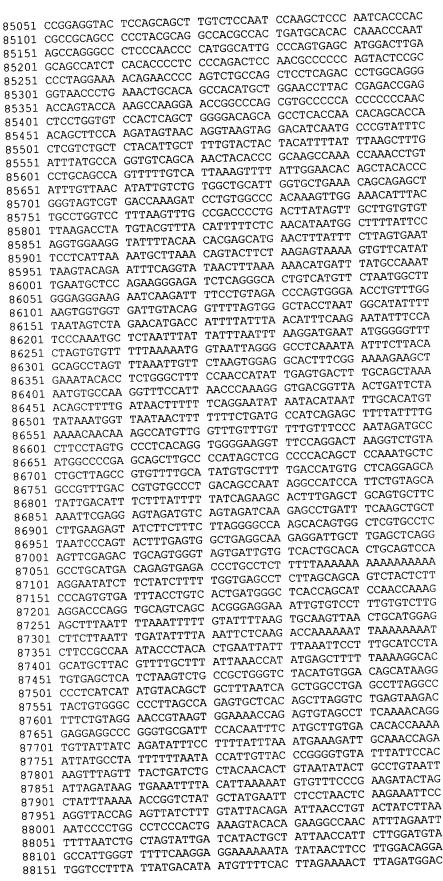


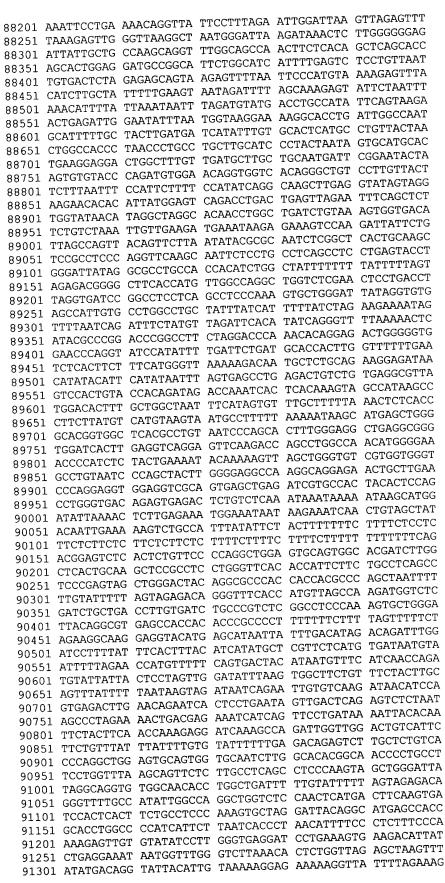


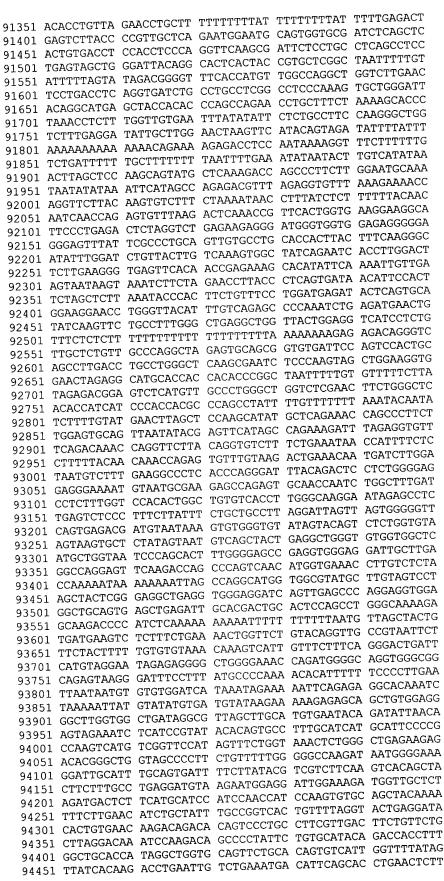


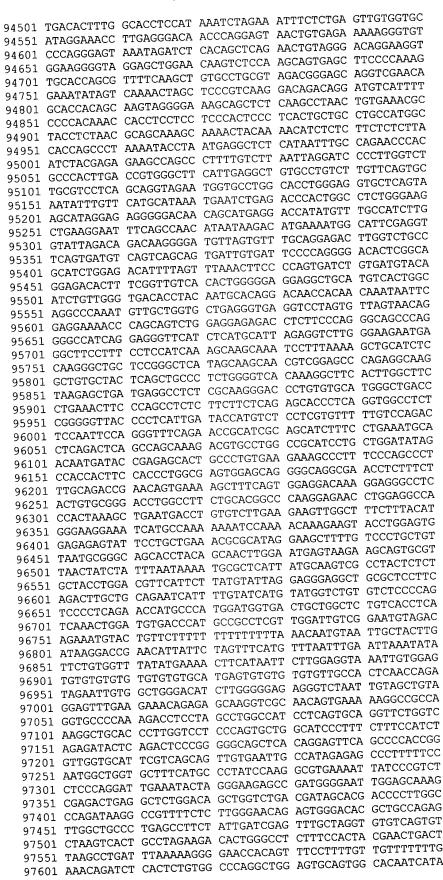


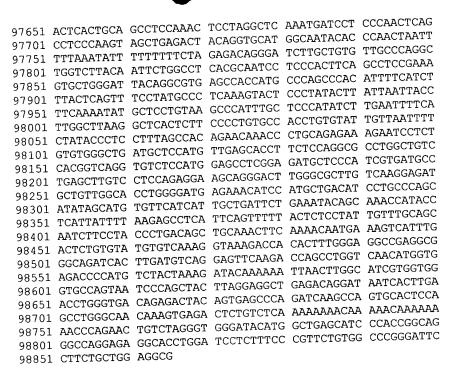












# FEATURES:

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Intron: 74265-80615 Exon: 80616-80785 Intron: 80786-84851 Exon: 84852-85472 Intron: 85473-95998 Exon: 95999-96126 Stop: 96127

# CHROMOSOME MAP POSITION:

Chromosome 16